```
                                    ┌── LIBRARY  1
                        SEQUENCES ──┼── LIBRARY  2
                        │           └── LIBRARY  "N"
                        │
                        │           ┌── LIBRARY  1
                        TRIMMED ────┼── LIBRARY  2
                        │           └── LIBRARY  "N"
                        │
                        │           ┌── LIBRARY  1
                        TRIMPARS ───┼── LIBRARY  2
                        │           └── LIBRARY  "N"
                        │
                        │           ┌── LIBRARY  1
                        HTML ───────┼── LIBRARY  2
                        │           └── LIBRARY  "N"
   ROOT ────────────────┤
                        │           ┌── LIBRARY  1
                        EXCEL ──────┼── LIBRARY  2
                        │           └── LIBRARY  "N"
                        │
                        │           ┌── LIBRARY  1.XLS  (FILE)
                        LIBRARY ────┼── LIBRARY  2.XLS  (FILE)
                        │           └── LIBRARY  "N".XLS  (FILE)
                        │
                        │
                        VECTORS
                        │
                        │
                        └── TEMP
```

FIG−1

Subtraction Library Utility

Choose the desired utility function

⊙ Select a Library

Known Subtraction Libraries

Create New
Library and
Associated
Directories

ralph
test
test1

○ Trim raw sequences

Known
Vector Files:

PCR-SELECT PRIMERS

Threshold: 80

○ Blast trimmed sequences

Available Databases to be searched

☐ est   ☐ yeast   ☐ htgs   ☐ vector
☑ nr   ☐ ecoli   ☐ pdb   ☑ kabat
☐ month   ☐ sts   ☐ alu   ☐ epd

Descriptions: 20

Alignments: 20

○ Create XLS files from blasted (HTML) sequence files

○ Update library from selected XLS files

Exit

Help

Select Files

0

files will be
processed

Go

Blast Later

☑ Sound

☑ Help Tips

Minimize

FIG-2

Confirm or Enter Trimming Positions

Insertion Orientation | Starting or 5' Adapter/Vector Information

	Sequence	Score	#	
Positive	AGCGGCCGCCCGGGCAGGT	68%	0	0
Negative	AGCGGTCGCGGGCCGAGGT	100%	0	0

Ending or 3' Adapter/Vector Information

	Sequence	Score	#	
	ACCTCGGCCCCGGACCACGCT	70%	0	0
	ACCTGCCCGGGCGGCCGCT	100%	0	0

TTAGCGGTGGTCGCGGGCCGAGGTACAGAACACTGACAAACAGGAAGAAAGACCTAGAAGGTTGTAGATGGGAAATCAGGAATGATTTGAACTGATAAAGATTTCGGA
CTCATAAGAACACATTTTAtnAATGTTAAACACAAAAACTACATGACTGAAGATGGATTTTATTACACATGGTGGAAGAGAAGAGGCCGTGTAGGTTTGCAAACAAA
GTTAAGAAATAGGAAACTGAATTTTCATTGTACAGAAAATGTATCTTCTTGGGAAGGCCTGTGTACCTGCCCGGGCGGCCTCGAAATTCCAGCACACTGCCGGCCGTTACTAGTTGGATCC
CANCTCGGTACCAAGCTTGGCGGTTATCATGGTCNTAANCTGTTTCCTGTGTGAAATTGTTATCCNCNCCCATTCCTCCCACNTTCCAACCTGAAACCTTAAATTTTAACCNCNGGGTGCCN
AATGAATNACCCACCCCNTTATGCTTTGCCNCCTGCCCCTCTCNTCNCCCCTCTTNTAAACCGGCNCNCCCNGGAAAGGTTTCTTTTGGCCCCTCCTCQCCCCTCCTNAT
CCTGCCCCT

5' ▽ △
3' ▽ △

\\Mricd-fs1\sweeneyre\Sub Lib Test\Sequence\test\41k06.seq

Length: 289 | Confirm Fwd: TTACTAGTGGATCCGAGCTTCGGTACCAAGCTT | 0%
Threshold: 80 | Confirm Rev: TTCGAACCATGGCTCGAGCC | 0%

Remove below base: 23
Remove above base: 312

☐ Allow Inserts   ☐ Positive Orientation
☑ Allow Deletes   ☑ Use Threshold

Sequencing direction was not determined

The current sequence was previously trimmed

[Find Best] [Back] [Apply] [Skip] [Abort All]

FIG-3